

PCT

WORLD INTELLECTUAL PROPERTY ORGANIZATION
International Bureau



INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

<p>(51) International Patent Classification ⁶ : C12N 15/29, 15/53, 15/82, 9/02, 5/10, A01H 1/00, 5/00</p>	<p>A2</p>	<p>(11) International Publication Number: WO 97/17447 (43) International Publication Date: 15 May 1997 (15.05.97)</p>
<p>(21) International Application Number: PCT/US96/18291 (22) International Filing Date: 7 November 1996 (07.11.96) (30) Priority Data: 60/006,315 7 November 1995 (07.11.95) US 60/023,502 6 August 1996 (06.08.96) US (71) Applicant: CALGENE, INC. [US/US]; 1920 Fifth Street, Davis, CA 95616 (US). (72) Inventors: YAMAMOTO, Harry, Y.; 716 Pao Street, Hon- olulu, HI 96825 (US). BUGOS, Robert, C.; 2135 Cham- berlain Street, Honolulu, HI 96822 (US). ROCKHOLM, David, C.; 1704 Anapuni Street, Honolulu, HI 96822 (US). (74) Agents: SCHWEDLER, Carl, J. et al.; Calgene, Inc., 1920 Fifth Street, Davis, CA 95616 (US).</p>		<p>(81) Designated States: CA, JP, MX, European patent (AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE). Published <i>Without international search report and to be republished upon receipt of that report.</i></p>
<p>(54) Title: PLANT VDE GENES AND METHODS RELATED THERETO (57) Abstract DNA sequences encoding plant vde enzymes are provided herein. The sequences may be joined to heterologous DNA sequences for use as probes and in DNA constructs to modify the genotype of a host organism. DNA constructs and methods are provided to modify a host cell phenotype by altering the amount of photoprotection enzyme present in the host cell. In plastid containing host cells, zeaxanthin levels and sensitivity to light can be modified through alterations in the level of vde enzymes.</p>		

FOR THE PURPOSES OF INFORMATION ONLY

Codes used to identify States party to the PCT on the front pages of pamphlets publishing international applications under the PCT.

AM	Armenia	GB	United Kingdom	MW	Malawi
AT	Austria	GE	Georgia	MX	Mexico
AU	Australia	GN	Guinea	NE	Niger
BB	Barbados	GR	Greece	NL	Netherlands
BE	Belgium	HU	Hungary	NO	Norway
BF	Burkina Faso	IE	Ireland	NZ	New Zealand
BG	Bulgaria	IT	Italy	PL	Poland
BJ	Benin	JP	Japan	PT	Portugal
BR	Brazil	KE	Kenya	RO	Romania
BY	Belarus	KG	Kyrgyzstan	RU	Russian Federation
CA	Canada	KP	Democratic People's Republic of Korea	SD	Sudan
CF	Central African Republic	KR	Republic of Korea	SE	Sweden
CG	Congo	KZ	Kazakhstan	SG	Singapore
CH	Switzerland	LI	Liechtenstein	SI	Slovenia
CI	Côte d'Ivoire	LK	Sri Lanka	SK	Slovakia
CM	Cameroon	LR	Liberia	SN	Senegal
CN	China	LT	Lithuania	SZ	Swaziland
CS	Czechoslovakia	LU	Luxembourg	TD	Chad
CZ	Czech Republic	LV	Latvia	TG	Togo
DE	Germany	MC	Monaco	TJ	Tajikistan
DK	Denmark	MD	Republic of Moldova	TT	Trinidad and Tobago
EE	Estonia	MG	Madagascar	UA	Ukraine
ES	Spain	ML	Mali	UG	Uganda
FI	Finland	MN	Mongolia	US	United States of America
FR	France	MR	Mauritania	UZ	Uzbekistan
GA	Gabon			VN	Viet Nam

PLANT VDE GENES AND METHODS RELATED THERETO**Field of the Invention**

This invention relates to genes encoding plant violaxanthin de-epoxidase (vde) and methods of use related to the protein and the nucleic acid sequences. The invention is exemplified by methods of causing increased expression or decreased expression of plant vde genes in plants. Included are plants produced by the method.

INTRODUCTION**Background**

Plant carotenoids are found in the membranes of chloroplasts and chromoplasts. They are instrumental in the photoprotective mechanisms of plants. Also, plant carotenoids have significant dietary implications. Thus, from an agronomic as well as a nutritional standpoint, study of the plant carotenoids and the enzymes involved in the biosynthesis of carotenoids is of interest.

Of particular interest are the late stages of the carotenoid biosynthetic pathway in plants, the xanthophyll cycle and its importance in photoregulation of photosynthesis. Photosynthesis is the process that enable plants to use light energy for growth and development. Thus, the availability of light of appropriate quality and quantity (photosynthetically active radiation or "PAR") is critical for plant growth and development. Ironically, light can also damage plants because plants have limited capacity to use light. When light intensity exceeds this capacity, irreversible damage can occur.

Plants have developed various mechanisms to cope with excess light such as varying leaf orientation or developing reflective surfaces. Such mechanisms appear to be specialized phenotypic strategies that are limited to certain types of plants. One mechanism that is apparently used by all plants

examined so far is the dissipation of excess energy as heat in the antenna (light absorbing structures) of the photosynthetic apparatus. Most of the excess energy is discarded as heat by a complex feed-back regulatory system that involves the transthylakoid ΔpH and formation of antheraxanthin and zeaxanthin catalyzed by violaxanthin de-epoxidase (vde) in the xanthophyll cycle. This system, termed energy dependent non-radiative energy dissipation or non-photochemical fluorescence quenching, reduces the quantum efficiency of photosystem II (PSII), helping to prevent PSII over reduction and photoinhibitory damage. In effect, this system provides a means to dump excess energy before it can damage the photosynthetic apparatus. The system has a wide dynamic range, both qualitatively and quantitatively, which enables it to function effectively over a wide-range of environmental conditions.

The ability to manipulate aspects of the xanthophyll cycle through genetic engineering techniques would permit the rapid introduction of improved plant varieties. However, it has been difficult to obtain purified fractions of the enzymes involved in the pathway and, prior to this invention, the corresponding genes have not been cloned.

SUMMARY OF THE INVENTION

DNA sequences encoding plant vde enzymes are provided herein. The sequences may be joined to heterologous DNA sequences for use as probes and in DNA constructs to modify the genotype of a host organism. DNA constructs and methods are provided to modify a host cell phenotype by altering the amount of photoprotection enzyme present in the host cell. In plastid containing host cells, zeaxanthin levels and sensitivity to light can be modified through alterations in the level of vde enzymes.

For example, over expression of vde is expected to increase the tolerance of plants to high light, drought and temperature stress (stress conditions exacerbate the condition of excess light). Also, plants that are not currently tolerant to high light or low temperatures are expected to become more tolerant

to these stresses. Plants that are better adapted to light stress are expected to be more productive and/or more resistant to disease. Alternatively, the under expression, or inhibition of vde activity is expected to increase photosynthetic efficiency under low light. The growing range of plants, crops, trees and ornamentals, could thus be modified.

Specific plant vde's are described. In particular, a 55 kD lettuce vde having the cDNA sequence and deduced amino acid sequence as shown in Fig. 1, a tobacco vde having the cDNA sequence and deduced amino acid sequence as shown in Fig. 2, and an *Arabidopsis* vde having the cDNA sequence and deduced amino acid sequence as shown in Fig. 3, are described. Figure 4 provides a comparison at the amino acid level of the proteins of Figures 1-3. In this amino acid sequence comparison the transit peptides for the three sequences are boxed. Identical amino acids are denoted by a hyphen. Gaps inserted to optimize sequence alignments are denoted with a period. The thirteen highly conserved cysteine residues are denoted with an asterisk.

Figure 5 is a comparison of the identity and similarity of pre-protein and mature protein vde. As can be seen from Figure 5, diverse vde's have sequences with about 75% sequence identity with one another at the amino acid level. Thus, vde sequences having at least about 75% homology to amino acid sequences in Fig.1, Fig.2 or Fig. 3 are also contemplated hereunder.

Nucleic acid sequences encoding a plant vde having at least about 60% sequence identity, and more preferably at least about 70% sequence identity, with the sequences in Figs. 1, 2 or 3, and are likewise contemplated herein. For instance, a comparison of tobacco and lettuce vde nucleic acid sequences give 76% identity, excluding the transit peptides. A high degree of sequence identity at the N-terminus is particularly preferred. Other related plant photoregulatory sequences having high degrees of similarity with fragments of the vde sequences shown are also contemplated.

In a different aspect of this invention, nucleic acid sequences related to the exemplified lettuce, tobacco and *arabidopsis* vde sequences of this invention are described with

details regarding methods to obtain such sequences from a variety of sources and their use. In addition, cDNA sequences encoding mature vde's are given as well as transit peptides, mRNA, genomic plant vdes, and plant vde regulatory regions.

In a further aspect of this invention, methods of producing vde in host cells are described. In plastid containing cells, modifications in the xanthophyll cycle, particularly in the ratio of violaxanthin as to zeaxanthin are contemplated via increased production of vde or decreased production of vde. This will have applications in the increased feed value of plants. Zeaxanthin levels are important to crops such as alfalfa whose value in part is due to xanthophyll content.

Results from studies of transgenic plants demonstrates that xanthophyll-mediated energy dissipation in LHCII apparently protects PSII against the potentially damaging effects of high light. This protection is induced by the combined effects of a thylakoid ΔpH and the presence of zeaxanthin and antheraxanthin formed by violaxanthin de-epoxidase (vde) activity.

DESCRIPTION OF THE FIGURES

FIG. 1 cDNA sequence for romaine lettuce vde and deduced polypeptide sequence. The underlined sequences are those determined from peptide sequencing of purified lettuce vde. The polypeptide sequence begins at the first methionine of the open reading frame and is preceded by three termination codons in the same reading frame.

FIG. 2 cDNA sequence for tobacco (*Nicotiana tabacum* cv. Xanthi) vde and deduced polypeptide sequence.

FIG. 3 cDNA sequence for *Arabidopsis thaliana* (var. columbia) vde and deduced polypeptide sequence.

FIG. 4 provides a comparison of the amino acid sequences of the proteins of Figures 1-3.

FIG. 5 shows the percent similarity between the the proteins of Figures 1-3.

FIG. 6 provides a comparison of hydropathy profiles for the vdes of three species.

FIG. 7 provides a time-course comparison of effects of expressed vde.

FIG. 8 is a table showing the results of pigment analysis of leaves of control and 18 vde-antisense tobacco plants (TAS-#).

FIG. 9 shows the results of a control plant extraction for vde.

FIG. 10 shows the results of extraction for vde in an antisense vde plant.

DETAILED DESCRIPTION OF THE INVENTION

A plant violaxanthin de-epoxidase or "vde" of this invention includes any sequence of amino acids, such as a protein, polypeptide or peptide, obtainable from a plant source, which demonstrates the ability to catalyze the production of zeaxanthin from violaxanthin under plant enzyme reactive conditions. By "enzyme reactive conditions" is meant that any necessary conditions that are available in an environment (i.e., such factors as temperature, pH, lack of inhibiting substances) which will permit the enzyme to function.

By "plant" is meant any plastid-containing organism. A "higher plant" shall mean any differentiated, multi-cellular plastid-containing organism. Of particular interest are plant vde's from angiosperms, both dicotyledonous and monocotyledonous plants.

In this invention, the cDNA sequence of a lettuce (Fig. 1), tobacco (Fig. 2) and *Arabidopsis* (Fig. 3) vde gene are provided. Transit peptide regions are identified in Fig. 4. From these sequences, genomic sequences may be obtained and the corresponding transcriptional and translational regulatory regions determined. Also, using the lettuce and/or tobacco sequences provided, vde genes from other sources may be obtained. In particular, it is found that the N-terminal regions of the lettuce, tobacco, *Arabidopsis* and spinach proteins are conserved and therefore, an N-terminal peptide such as "VDALKTCACLLK" will find particular use in obtaining related sequences.

Constructs for use in the methods may include several forms, depending upon the intended use of the construct. Thus, the constructs include vectors, transcriptional cassettes, expression cassettes and plasmids. The transcriptional and translational initiation region (also sometimes referred to as a "promoter") preferably comprises a transcriptional initiation regulatory region and a translational initiation regulatory region of untranslated 5' sequences, "ribosome" binding sites, responsible for binding mRNA to ribosomes and translational initiation. It is preferred that all of the transcriptional and translational functional elements of the initiation control region are derived from or obtainable from the same gene. In some embodiments, the promoter will be modified by the addition of sequences, such as enhancers, or deletions of nonessential and/or undesired sequences. By "obtainable" is intended a promoter having a DNA sequence sufficiently similar to that of a native promoter to provide for the desired specificity of transcription of a DNA sequence of interest. It includes natural and synthetic sequences as well as sequences which may be a combination of synthetic and natural sequences.

A transcriptional cassette for transcription of a nucleotide sequence of interest will include in the direction of transcription, a transcription initiation region and optionally a translational initiation region, a DNA sequence of interest, and a transcriptional and optionally translational termination region functional in the host cell of interest. When the cassette provides for the transcription and translation of a DNA sequence it is considered an expression cassette. One or more introns may also be present. Other sequences may also be present, including those encoding transit peptides.

The use of amino acid sequences from vde peptides to obtain nucleic acid sequences which encode lettuce vde is described herein. For example, synthetic oligonucleotides are prepared which correspond to the vde peptide sequences. The oligonucleotides are used as primers in polymerase chain reaction (PCR) techniques to obtain partial DNA sequence of vde genes. The partial sequences so obtained are then used as

probes to obtain vde clones from a gene library prepared from lettuce tissue. Alternatively, where oligonucleotides of low degeneracy can be prepared from particular vde peptides, such probes may be used directly to screen gene libraries for vde gene sequences. In particular, screening of cDNA libraries in phage vectors is useful in such methods due to lower levels of background hybridization.

A nucleic acid sequence of a plant vde of this invention may be a DNA or RNA sequence, derived from genomic DNA, cDNA, mRNA, or may be synthesized in whole or in part. The gene sequences may be cloned, for example, by isolating genomic DNA from an appropriate source, and amplifying and cloning the sequence of interest using a polymerase chain reaction (PCR). Alternatively, the gene sequences may be synthesized, either completely or in part, especially where it is desirable to provide plant-preferred sequences. Thus, all or a portion of the desired structural gene (that portion of the gene which encodes the vde protein) may be synthesized using codons preferred by a selected host. Host-preferred codons may be determined, for example, from the codons used most frequently in the proteins expressed in a desired host species.

One skilled in the art will readily recognize that antibody preparations, nucleic acid probes (DNA and RNA) and the like may be prepared and used to screen and recover "homologous" or "related" vde's from a variety of plant sources. Homologous sequences are found when there is an identity of sequence, which may be determined upon comparison of sequence information, nucleic acid or amino acid, or through hybridization reactions between a known vde and a candidate source. Conservative changes, such as Glu/Asp, Val/Ile, Ser/Thr, Arg/Lys and Gln/Asn may also be considered in determining sequence homology. Amino acid sequences are considered homologous by as little as 25% sequence identity between the two complete mature proteins. (See generally, Doolittle, R.F., *OF URFS and ORFS* (University Science Books, CA, 1986.)

Thus, other plant vde's may be obtained from the specific exemplified lettuce, tobacco and *Arabidopsis* sequences provided

herein. Furthermore, it will be apparent that one can obtain natural and synthetic plant vde's, including modified amino acid sequences and starting materials for synthetic-protein modeling from the exemplified plant vde's and from plant vde's which are obtained through the use of such exemplified sequences.

Modified amino acid sequences include sequences which have been mutated, truncated, increased and the like, whether such sequences were partially or wholly synthesized. Sequences which are actually purified from plant preparations or are identical or encode identical proteins thereto, regardless of the method used to obtain the protein or sequence, are equally considered naturally derived.

Typically, a plant vde sequence obtainable from the use of nucleic acid probes will show 60-70% sequence identity between the target vde sequence and the encoding sequence used as a probe. However, lengthy sequences with as little as 50-60% sequence identity may also be obtained. The nucleic acid probes may be a lengthy fragment of the nucleic acid sequence, or may also be a shorter, oligonucleotide probe. When longer nucleic acid fragments are employed as probes (greater than about 100 bp), one may screen at lower stringencies in order to obtain sequences from the target sample which have 20-50% deviation (i.e., 50-80% sequence homology) from the sequences used as probe. Oligonucleotide probes can be considerably shorter than the entire nucleic acid sequence encoding a vde enzyme, but should be at least about 10, preferably at least about 15, and more preferably at least about 20 nucleotides. A higher degree of sequence identity is desired when shorter regions are used as opposed to longer regions. It may thus be desirable to identify regions of highly conserved amino acid sequence to design oligonucleotide probes for detecting and recovering other related vde genes. Shorter probes are often particularly useful for polymerase chain reactions (PCR), especially when highly conserved sequences can be identified. (See, Gould, et al., *PNAS USA* (1989) 86:1934-1938.)

To determine if a related gene may be isolated by hybridization with a given sequence, the sequence is labeled to

allow detection, typically using radioactivity, although other methods are available. The labeled probe is added to a hybridization solution, and incubated with filters containing the desired nucleic acids, either Northern or Southern blots (to screen desired sources for homology), or the filters containing cDNA or genomic clones to be screened. Hybridization and washing conditions may be varied to optimize the hybridization of the probe to the sequences of interest. Lower temperatures and higher salt concentrations allow for hybridization of more distantly related sequences (low stringency). If background hybridization is a problem under low stringency conditions, the temperature can be raised either in the hybridization or washing steps and/or salt content lowered to improve detection of the specific hybridizing sequence. Hybridization and washing temperatures can be adjusted based on the estimated melting temperature of the probe as discussed in Beltz, et al. (*Methods in Enzymology* (1983) 100:266-285).

A useful probe and appropriate hybridization and washing conditions having been identified as described above; cDNA or genomic libraries are screened using the labeled sequences and optimized conditions. The libraries are first plated onto a solid agar medium, and the DNA lifted to an appropriate membrane, usually nitrocellulose or nylon filters. These filters are then hybridized with the labeled probe and washed as discussed above to identify clones containing the related sequences. When a genomic library is used, one or more sequences may be identified providing both the coding region and the transcriptional regulatory elements of the vde gene from such plant source.

For immunological screening, antibodies to the vde protein can be prepared by injecting rabbits or mice with the protein purified from the original plant source or expressed from a host cell, such methods of preparing antibodies being well known to those in the art. Either monoclonal or polyclonal antibodies can be produced, although typically polyclonal antibodies are more useful for gene isolation. Western analysis may be conducted to determine that a related protein is present in a

crude extract of the desired plant species, as determined by cross-reaction with the antibodies to the vde. When cross-reactivity is observed, genes encoding the related proteins are isolated by screening expression libraries representing the desired plant species. Expression libraries can be constructed in a variety of commercially available vectors, including lambda gt11, as described in Maniatis, et al. (*supra*).

All plants studied to date utilize the xanthophyll cycle, and thus any given plant species can be considered as a source of additional vde proteins.

The nucleic acid sequences associated with plant vde proteins will find many uses. For example, recombinant constructs can be prepared which can be used as probes or will provide for expression of the vde protein in host cells to produce a ready source of the enzyme. Other useful applications may be found when the host cell is a plant host cell, either *in vitro* or *in vivo*. For example, by increasing the amount of a respective vde available to the plant xanthophyll cycle, an increased percentage of zeaxanthin may be obtained. In a like manner, for some applications it may be desired to decrease the amount of vde endogenously expressed in a plant cell by antisense or some other reducing technology such as co-suppression. For example, to improve photosynthetic efficiency of a plant under low light, decreased expression of a vde may be desired.

Thus, depending upon the intended use, the constructs may contain the sequence which encodes the entire vde protein, or a portion thereof. For example, where antisense inhibition of a given vde protein is desired, the entire vde sequence is not required. Furthermore, where vde constructs are intended for use as probes, it may be advantageous to prepare constructs containing only a particular portion of an vde encoding sequence, for example a sequence which is discovered to encode a highly conserved vde region.

As discussed above, nucleic acid sequence encoding a plant vde of this invention may include genomic, cDNA or mRNA sequence. By "encoding" is meant that the sequence corresponds to a particular amino acid sequence either in a sense or anti-

sense orientation. By "extrachromosomal" is meant that the sequence is outside of the plant genome of which it is naturally associated. By "recombinant" is meant that the sequence contains a genetically engineered modification through manipulation via mutagenesis, restriction enzymes, and the like.

A cDNA sequence may or may not contain pre-processing sequences, such as transit peptide sequences or targeting sequences to facilitate delivery of the vde protein to a given organelle or membrane location. The use of any such precursor vde DNA sequences is preferred for uses in plant cell expression. A genomic vde sequence may contain the transcription and translation initiation regions, introns, and/or transcript termination regions of the plant vde, which sequences may be used in a variety of DNA constructs, with or without the vde structural gene. Thus, nucleic acid sequences corresponding to the plant vde of this invention may also provide signal sequences useful to direct protein delivery into a particular organelle or membrane location, 5' upstream non-coding regulatory regions (promoters) having useful tissue and timing profiles, 3' downstream non-coding regulatory region useful as transcriptional and translational regulatory regions and may lend insight into other features of the gene.

Once the desired plant vde nucleic acid sequence is obtained, it may be manipulated in a variety of ways. Where the sequence involves non-coding flanking regions, the flanking regions may be subjected to resection, mutagenesis, etc. Thus, transitions, transversions, deletions, and insertions may be performed on the naturally occurring sequence. In addition, all or part of the sequence may be synthesized. In the structural gene, one or more codons may be modified to provide for a modified amino acid sequence, or one or more codon mutations may be introduced to provide for a convenient restriction site or other purpose involved with construction or expression. The structural gene may be further modified by employing synthetic adapters, linkers to introduce one or more convenient restriction sites, or the like.

The nucleic acid or amino acid sequences encoding a plant vde of this invention may be combined with other non-native, or "heterologous", sequences in a variety of ways. By "heterologous" sequences is meant any sequence which is not naturally found joined to the plant vde, including, for example, combinations of nucleic acid sequences from the same plant which are not naturally found joined together.

The DNA sequence encoding a plant vde of this invention may be employed in conjunction with all or part of the gene sequences normally associated with the vde. In its component parts, a DNA sequence encoding vde is combined in a DNA construct having, in the 5' to 3' direction of transcription, a transcription initiation control region capable of promoting transcription and translation in a host cell, the DNA sequence encoding plant vde and a transcription and translation termination region.

Potential host cells include both prokaryotic and eukaryotic cells. A host cell may be unicellular or found in a multicellular differentiated or undifferentiated organism depending upon the intended use. Cells of this invention may be distinguished by having a plant vde foreign to the wild-type cell present therein, for example, by having a recombinant nucleic acid construct encoding a plant vde therein.

Depending upon the host, the regulatory regions will vary, including regions from viral, plasmid or chromosomal genes, or the like. For expression in prokaryotic or eukaryotic microorganisms, particularly unicellular hosts, a wide variety of constitutive or regulatable promoters may be employed. Expression in a microorganism can provide a ready source of the plant enzyme. Among transcriptional initiation regions which have been described are regions from bacterial and yeast hosts, such as *E. coli*, *B. subtilis*, *Saccharomyces cerevisiae*, including genes such as beta-galactosidase, T7 polymerase, tryptophan E and the like.

For the most part, the constructs will involve regulatory regions functional in plants. The open reading frame, coding for the plant vde or functional fragment thereof will be joined

at its 5' end to a transcription initiation regulatory region such as the wild-type sequence naturally found 5' upstream to the vde structural gene. Numerous other transcription initiation regions are available which provide for a wide variety of constitutive or regulatable, e.g., inducible, transcription of the structural gene functions. Constitutive promoters such as the CaMV 35S promoter, double 35S promoter, 34S figwort promoter may be useful. Promoters which express in plastid containing cells will be of special interest. Some such promoters are preferentially expressed in plastid containing tissues, such as the ssu promoter. The transcription/translation initiation regions corresponding to such structural genes are found immediately 5' upstream to the respective start codons. In embodiments wherein the expression of the vde protein is desired in a plant host, the use of all or part of the complete plant vde gene is desired; namely all or part of the 5' upstream non-coding regions (promoter) together with the structural gene sequence and 3' downstream non-coding regions may be employed. If a different promoter is desired, such as a promoter native to the plant host of interest or a modified promoter, i.e., having transcription initiation regions derived from one gene source and translation initiation regions derived from a different gene source, including the sequence encoding the plant vde of interest, or enhanced promoters, such as double 35S CaMV promoters, the sequences may be joined together using standard techniques.

Expression of the vde transcript was followed in market romaine lettuce leaves that were dark adapted for an undetermined period of time. The same level of transcript was detected in both yellow leaves and rapidly expanding green leaves. However, a greater transcript level was detected in mature green leaves. Two hybridizing transcripts were observed for each sample indicating the possibility that the upper larger transcript may be processed to the slightly smaller transcript (1.7 kb) having the greater level of hybridization. The increased level of transcript in mature green leaves of lettuce may be due to two possible reasons: higher expression occurs in

tissues with a higher density of fully developed chloroplasts or expression may be regulated by light intensity since the mature green leaves receive a higher intensity of light than the immature leaves which are partially shielded in the center of the head of lettuce. Hence, use of the vde promoter may be particularly useful in the transcription of vde nucleic acid sequences or for the expression of other nucleic acid sequences of interest.

Regulatory transcript termination regions may be provided in DNA constructs of this invention as well. Transcript termination regions may be provided by the DNA sequence encoding the plant vde or a convenient transcription termination region derived from a different gene source, for example, the transcript termination region which is naturally associated with the transcript initiation region. Where the transcript termination region is from a different gene source, it will contain at least about 0.5 kb, preferably about 1-3 kb of sequence 3' to the structural gene from which the termination region is derived.

Plant expression or transcription constructs having a plant vde as the DNA sequence of interest for increased or decreased expression thereof may be employed with a wide variety of plant life, particularly, plant life where light regulation or zeaxanthin levels are important. Plants of interest include, but are not limited to ornamental plant varieties, field and forage crops, including alfalfa and trees. Depending on the method for introducing the recombinant constructs into the host cell, other DNA sequences may be required. Importantly, this invention is applicable to dicot and monocot species alike and will be readily applicable to new and/or improved transformation and regulation techniques.

The method of transformation in obtaining such transgenic plants is not critical to the instant invention, and various methods of plant transformation are currently available. Furthermore, as newer methods become available to transform crops, they may also be directly applied hereunder. For example, many plant species naturally susceptible to

Agrobacterium infection may be successfully transformed via tripartite or binary vector methods of *Agrobacterium* mediated transformation. In many instances, it will be desirable to have the construct bordered on one or both sides by T-DNA, particularly having the left and right borders, more particularly the right border. This is particularly useful when the construct uses *A. tumefaciens* or *A. rhizogenes* as a mode for transformation, although the T-DNA borders may find use with other modes of transformation. In addition, techniques of microinjection, DNA particle bombardment, and electroporation have been developed which allow for the transformation of various monocot and dicot plant species.

Normally, included with the DNA construct will be a structural gene having the necessary regulatory regions for expression in a host and providing for selection of transformant cells. The gene may provide for resistance to a cytotoxic agent, e.g. antibiotic, heavy metal, toxin, etc., complementation providing prototrophy to an auxotrophic host, viral immunity or the like. Depending upon the number of different host species the expression construct or components thereof are introduced, one or more markers may be employed, where different conditions for selection are used for the different hosts.

Where *Agrobacterium* is used for plant cell transformation, a vector may be used which may be introduced into the *Agrobacterium* host for homologous recombination with T-DNA or the Ti- or Ri-plasmid present in the *Agrobacterium* host. The Ti- or Ri-plasmid containing the T-DNA for recombination may be armed (capable of causing gall formation) or disarmed (incapable of causing gall formation), the latter being permissible, so long as the vir genes are present in the transformed *Agrobacterium* host. The armed plasmid can give a mixture of normal plant cells and gall.

In some instances where *Agrobacterium* is used as the vehicle for transforming host plant cells, the expression or transcription construct bordered by the T-DNA border region(s) will be inserted into a broad host range vector capable of

replication in *E. coli* and *Agrobacterium*, there being broad host range vectors described in the literature. Commonly used is pRK2 or derivatives thereof. See, for example, Ditta, et al., (Proc. Nat. Acad. Sci., U.S.A. (1980) 77:7347-7351) and EPA 0 120 515, which are incorporated herein by reference.

Alternatively, one may insert the sequences to be expressed in plant cells into a vector containing separate replication sequences, one of which stabilizes the vector in *E. coli*, and the other in *Agrobacterium*. See, for example, McBride and Summerfelt (Plant Mol. Biol. (1990) 14:269-276), wherein the pRiHRI (Jouanin, et al., Mol. Gen. Genet. (1985) 201:370-374) origin of replication is utilized and provides for added stability of the plant expression vectors in host *Agrobacterium* cells.

Included with the expression construct and the T-DNA will be one or more markers, which allow for selection of transformed *Agrobacterium* and transformed plant cells. A number of markers have been developed for use with plant cells, such as resistance to chloramphenicol, kanamycin, the aminoglycoside G418, hygromycin, or the like. The particular marker employed is not essential to this invention, one or another marker being preferred depending on the particular host and the manner of construction.

For transformation of plant cells using *Agrobacterium*, explants may be combined and incubated with the transformed *Agrobacterium* for sufficient time for transformation, the bacteria killed, and the plant cells cultured in an appropriate selective medium. Once callus forms, shoot formation can be encouraged by employing the appropriate plant hormones in accordance with known methods and the shoots transferred to rooting medium for regeneration of plants. The plants may then be grown to seed and the seed used to establish repetitive generations.

The invention now being generally described, it will be more readily understood by reference to the following examples which are included for purposes of illustration only and are not intended to limit the present invention.

EXAMPLES

Example 1 - Lettuce vde cDNA

Vde was purified from romaine lettuce (*Lactuca sativa* L. cv Romaine) chloroplasts and peptides from a tryptic digest along with the N-terminus were sequenced (Rockholm, *Plant Physiol.* (1996) 110:697-703). Two peptides (N-terminus and tryptic fragment #15, shown in Fig.1) were used to develop the oligonucleotides

5'-GAYGCHYTBAAGACHTGYGC-3' (216-fold degeneracy) and

5'TTGVARRTTDGGRATRAT-3' (144-fold degeneracy).

The partial cDNA for vde was amplified by 35 cycles of polymerase chain reaction (PCR) containing 25 pmol of each primer and lettuce cDNA using an annealing temperature of 50°C. The PCR product was subcloned into pGEM-7Zf (Promega) by blunt-end cloning and sequenced. A cDNA library was constructed from poly(A)+ RNA isolated from a pooled sample of various age romaine lettuce leaves using the Timesaver cDNA Synthesis Kit (Pharmacia) and ligated into lambda-ZAPII (Stratagene). A total of 2.5×10^5 recombinant plaques were screened with the PCR product labeled by random priming and positive clones were plaque purified followed by *in vivo* excision of the plasmid. The cDNAs were subcloned into the *Not*I site of pGEM-5Zf and both strands of cDNA were sequenced completely using an Applied Biosystems Model 373A automated sequencer. The Genbank accession number is U31462.

The vde cDNA encompasses an open reading frame encoding a 473 amino acid protein with a calculated *Mr* of 54,447. The deduced protein contains an 125 amino acid putative transit peptide for transport into the chloroplast lumen where the enzyme is localized (Hager, *Planta* (1969)89:224-243). This was verified by *in vitro* transcription/translation of two vde (vde1:-234 to 1526 bp and vde2:-65 to 1578 bp of Fig. 1) cDNAs which produced a 55 Kd product on a sodium dodecyl sulfate (SDS)-polyacrylamide gel. The N-terminus of the mature vde

protein (amino acid #126) was determined by N-terminal sequencing of purified vde from romaine lettuce. Therefore, mature vde consists of a 348 amino acid protein with a calculated Mr of 39,929 and a calculated pI of 4.57.

The primary structure of the deduced mature vde exhibits some characteristic features. The protein is hydrophilic overall with 57.2% of the total amino acid residues having polar side chains. Three interesting domains were identified in the deduced mature vde including a cysteine rich domain, a lipocalin signature and a highly charged domain. In the first domain 11 of the 13 total cysteines in the mature vde are present suggesting that this is most likely the site where dithiothreitol (DTT), a known inhibitor of vde, has its effect. The cysteines probably form more than one disulfide linkage since partial inhibition of vde activity with DTT results in an accumulation of antheraxanthin. The deduced mature vde also contains a lipocalin signature, a domain identified in a number of diverse proteins that bind small hydrophobic molecules. For example, crustacyanin, a protein from lobster carapace which contains a lipocalin signature, binds the carotenoid astaxanthin. Similarly, this domain may play a role in binding the substrate violaxanthin. In the third domain approximately 47% of the residues have charged side chains. The most striking feature of this domain is the high concentration of glutamic acid residues; 27.6% of the residues in this domain (69.2% of the total in the mature vde) are glutamic acids whereas only 2% are aspartic acids.

Figure 4 provides a detailed analysis of the deduced amino acid sequence of vde. The top portion provides a comparison of the deduced amino acid sequences of vde from three plant species. The transit peptides are located in the boxed region. Identical residues are indicated by hyphens (-). Gaps introduced to maximize sequence alignment are indicated by periods (.). Asterisks (*) identify the 13 cysteine residues that are conserved between the three sequences.

The bottom map of Figure 4 shows the three domains identified. The amino acid spanning regions for lettuce vde are indicated below the domains.

Figure 6 provides hydropathy profiles for the vdes from three species.

Example 2 - Expression of Lettuce vde cDNA in E.coli

Authenticity of the lettuce vde cDNA was confirmed by expression of the fragment vde2 in *E. coli*. Vde2 was subcloned in both sense and antisense orientations with respect to *lacZ* into the *NotI* site of pGEM-5Zf and transformed into *E. coli* DH5alpha. All cultures were incubated and induced with 10 mM IPTG (Bugos, *Plant Mol Biol.* (1991)17:1203-1215). Following the 2 hr induction, the cells were centrifuged at 4000xg for 10 min at 4°C. The cells were resuspended in 3 ml 50 mM Tris (pH 7.4), 1 mM EDTA and lysed using an ultrasonic cell disrupter equipped with a micro-probe for 10 cycles (30 sec on/30 sec off) while being cooled in an ice bath. The resulting extract was centrifuged at 10,000xg for 10 min at 4°C and the supernatant was collected for determining vde activity using the *in vitro* assay and absorbance change at 502nm minus 540nm (Yamamoto, *Methods Enzymol.* (1985)110:303-312). The pellet was washed with 3 ml 50 mM Tris (pH 7.4), 1 mM EDTA and centrifuged. The pellet was resuspended in 3 ml buffer and assayed. All assays contained 100 µl *E. coli* extract or pellet resuspension. For quantification of xanthophyll pigments, the reactions were stopped at various times with addition of solid Tris and the xanthophylls were extracted 3 times with diethyl ether. The ether was dried under a stream of N₂ and the xanthophylls were solubilized in 100 µl 90% acetone followed by HPLC analysis (Gilmore, *J. Chromatogr.* (1991)543:137-145).

Extracts from *E. coli* expressing the fragment orientated with *lacZ* (sense) had strong vde activity whereas no detectable activity was observed from extracts of *E. coli* transformed with vde2 in antisense orientation or pGEM-5Zf alone. Furthermore, addition of DTT, a strong inhibitor of de-epoxidase activity, abolished all vde activity. DTT (3mM, final conc.) was added

directly to the assay 50 seconds after ascorbate (30mM, final conc.) addition. Specific activity of the enzyme was 64.9 ± 5.4 nmols violaxanthin deepoxidized/min/mg protein. Trace activity was detected in the membrane fraction of vde2 sense suggesting that some of the enzyme was not washed away following lysis or that lysis was not complete. An attempt to express the vde1 fragment was unsuccessful. *E. coli* transformed with vde1 subcloned in pGEM-5Zf and orientated with lacZ did not grow.

To verify the products of de-epoxidation, the reaction with vde2 sense extract was stopped at various times and the xanthophylls were analyzed by HPLC. Antheraxanthin and zeaxanthin appeared consistent with sequential de-epoxidation and concomitant with the rapid decrease in violaxanthin, similar to observations reported over three decades earlier for de-epoxidation in lima bean (*Phaseolus leunatus*) leaves exposed to high light (Yamamoto, *Arch. Biochem. Biophys.* (1962)97:168-173). The specific activity of the enzyme was 19.4 ± 0.9 nmols violaxanthin de-epoxidized/min/mg protein. This is the first unequivocal evidence that the same enzyme catalyzes the two-step mono de-epoxidation reaction.

Example 3 - vde in Other Plants

Western analysis of vde from chloroplasts of various C_3 plants and expressed vde in *E. coli* demonstrate that the N-terminus is conserved.

Intact chloroplasts were isolated (Neubauer, *Plant Physiol.* (1992)99:1354-1361) and lysed with five freeze/thaw cycles using liquid N_2 (Hager, *Planta* (1975)88:27-44). Expression of vde2 in *E. coli* DH5-alpha was as described in Example 2 and the cells were lysed using the freeze/thaw method. Proteins were resolved on a 12% SDS-polyacrylamide gel and electrophoretically transferred to PVDF. Color development was performed following incubation with alkaline phosphatase-conjugated secondary antibodies. Protein was estimated using a prepared reagent (Biorad) and bovine gamma globulin as the standard.

The blot was probed with a polyclonal antibody prepared against a synthetic peptide derived from the N-terminus of

lettuce vde (VDALKTCACLLK). Vde migrates with an approximate size of 43 kD.

The mature vde from market romaine lettuce, tobacco (*Nicotiana tabacum* L. cv Xanthi) and market spinach (*Spinacia oleracea* L.) all migrate with approximately the same M_r of 43K. The antibody recognized vde in these three plant species demonstrating that the N-terminus is conserved. Expressed vde2 in *E. coli* migrated at the same M_r as the romaine lettuce vde whereas extracts from *E. coli* containing only pGEM-5Zf produce some minor cross-reacting proteins, none of which having a M_r of 43K. The M_r 's of the above vde proteins are in agreement with the calculated M_r of the deduced mature vde (39.9K). Two interesting observations are evident from vde expressed in *E. coli*. The first is that the *E. coli* expressed vde produced many immunoreactive bands of lower molecular weight. Reasons for this may be due to some processing occurring at the C-terminus of the protein by *E. coli* (since the antibody recognizes the N-terminus) or due to translational pausing. The second is that the bacterial expressed vde protein migrates at the same molecular weight as mature vde from romaine lettuce and not as the expected size of the deduced vde preprotein (54.4K) with the transit peptide. This suggests that *E. coli* may recognize the chloroplast transit peptide and cleave it. The N-terminus of the bacterial expressed vde will need to be sequenced to determine the actual site where cleavage is occurring. A similar observation was also reported for the nuclear-encoded chloroplast enzyme acetolactate synthase from *Arabidopsis* when expressed in *E. coli*.

Figure 7 shows the kinetics of absorbance change demonstrating expression of active violaxanthin de-epoxidase in *E. coli* DH5 (top of Fig. 7). Expression was assayed from vde2 constructs in both sense and antisense orientations with respect to *lacZ* along with *E. coli* containing the vector only (pGEM-5Zf). DTT (3mM, final concentration) was added directly to the assay 70 seconds after ascorbate (30 mM, final concentration) addition. Specific activity of the enzyme was 64.9 ± 5.4 nmols violaxanthin de-epoxidized min⁻¹ mg. protein⁻¹.

The bottom of Figure 7 is a timecourse of xanthophyll conversions by expressed vde2 (sense construct) in *E. coli*. Specific activity of the enzyme was 19.4 ± 0.9 nmols violaxanthin de-epoxidized min⁻¹ protein⁻¹.

Example 4 - Effects of Expression of vde in Plants

In Figure 8, pigment analysis of leaves of 212 control tobacco plants (Ct-#) is provided, as well as the mean percentage of violaxanthin which is de-epoxidized. Also provided by Figure 8 is the pigment analysis of leaves of 18 vde-antisense tobacco plants (TAS-#).

Tobacco plants were transformed with an antisense construct of the tobacco vde cDNA under control of the CaMV 35S promoter (pB1121) using *Agrobacterium tumefaciens* LBA4404. A total of 40 antisense plants were analyzed with 18 showing various levels of inhibition of de-epoxidation.

Relative pigment concentration for tobacco (*Nicotiana tabacum* L. cv. Xanthi) leaves was measured by leaf disks punched from tobacco leaves that were dark adapted for a few hours. One leaf disk (dark adapted) was extracted with acetone and analyzed by HPLC while another was light induced by exposing the disk to 1800 $\mu\text{mol m}^{-2} \text{s}^{-1}$ white light for 20 min while the leaf disk was floating on water in a water-jacketed beaker cooled at 20°C. Following the light treatment, the leaf disk was extracted and analyzed by HPLC.

Two vde-antisense tobacco plants (TAS-32 and TAS-39) were recovered that had undetectable levels of zeaxanthin following illumination with bright white light. Low levels of antheraxanthin (~2-3%) were present in some dark-adapted leaves and are assumed to represent incomplete epoxidase activity.

In Figures 9 and 10, results are provided from a comparison of measurements on a tobacco leaf from a control plant (Ct-30) and a vde-antisense plant (TAS-5), both of which were dark adapted for 24 hours. Under low light conditions, three leaf disks were punched from each leaf. One leaf disk (dark adapted) was extracted and analyzed by HPLC.

The remaining two leaf disks were pre-illuminated with 500 $\mu\text{mol m}^{-2} \text{s}^{-1}$ red light for 15 minutes. One of these disks was then extracted and analyzed by HPLC while the other was placed in the dark for 10 minutes prior to fluorometry and HPLC analysis.

It has also been observed that in tobacco plants where lettuce vde has been overexpressed from a 35S construct, flowering is delayed, and flowers are slightly larger.

CLAIMS

What is claimed is:

1. An isolated DNA sequence encoding plant violaxanthin de-epoxidase.
2. The DNA sequence of Claim 1 wherein said violaxanthin de-epoxidase DNA sequence is joined to a heterologous nucleic acid sequence.
3. A recombinant DNA construct capable of directing the transcription of RNA in a plant cell, wherein said construct comprises in the order of transcription, a plant transcription initiation region, the violaxanthin de-epoxidase encoding sequence of Claim 1, and a transcriptional termination region.
4. The DNA sequence of Claim 1 having at least about 70% homology at the DNA level to a sequence selected from the group consisting of the nucleic acid sequences shown in Fig. 1, Fig. 2 and Fig. 3.
5. The DNA sequence of Claim 4, wherein said sequence is selected from the group consisting of the nucleic acid sequences in Fig. 1, Fig. 2 and Fig. 3.
6. The DNA sequence of Claim 1, wherein said sequence encodes at least about the twenty N-terminus amino acids of a protein selected from the group consisting of the plant violaxanthin de-epoxidase proteins in Fig. 1, Fig. 2 and Fig. 3.
7. The DNA sequence of Claim 6, wherein said sequence encodes a plant violaxanthin de-epoxidase protein selected from the group consisting of the proteins in Fig. 1, Fig. 2 and Fig. 3.

8. The DNA sequence of Claim 1, wherein said sequence encodes the amino acids VDALKTCACLLK.
9. A method of modifying the violaxanthin de-epoxidase levels in a plant, said method comprising growing a plant transformed by a construct according to Claim 3.
10. The method of Claim 9 wherein said encoding sequence is in sense orientation.
11. The method of Claim 10 wherein said construct further comprises a plastid translocation sequence.
12. The method of Claim 9 wherein said encoding sequence is in an antisense orientation with respect to regulatory elements in said construct.
13. A method of modifying the sensitivity of a transgenic plant to light comprising growing a plant transformed by a construct according to Claim 3.
14. The method of Claim 11 wherein violaxanthin de-epoxidase activity is increased resulting in increased zeaxanthin and antheraxanthin production.
15. The method of Claim 12 wherein violaxanthin de-epoxidase activity is decreased resulting in decreased zeaxanthin and antheraxanthin levels in said plant.
16. The method of Claim 14 wherein said increased zeaxanthin and antheraxanthin levels results in said plant being tolerant of increased light levels, as opposed to a non-transformed control plant of the same type.
17. The method of Claim 15 wherein said decreased zeaxanthin and antheraxanthin levels results in said plant being

intolerant of light levels which are tolerated by a non-transformed control plant of the same type.

18. A transgenic plant with modified sensitivity to light as a consequence of the activity of an introduced construct which operates to alter the zeaxanthin or antheraxanthin levels in cells of said transgenic plant.

19. A plant, plant cell or other plant part comprising a construct according to Claim 3.

20. A plant, plant cell or other plant part produced by the method of Claim 9.

21. A plant, plant cell or other plant part produced by the method of Claim 11 wherein flowering of said plant is delayed as compared to flowering in a control plant not produced by said method.

22. A plant, plant cell or other plant part produced by the method of Claim 11 wherein flowers of said plant are larger as compared to flowers of a control plant not produced by said method.

```

155
156
157
158
159
160
161
162
163
164
165
166
167
168
169
170
171
172
173
174
175
176
177
178
179
180
181
182
183
184
185
186
187
188
189
190
191
192
193
194
195
196
197
198
199
200
201
202
203
204
205
206
207
208
209
210
211
212
213
214
215
216
217
218
219
220
221
222
223
224
225
226
227
228
229
230
231
232
233
234
235
236
237
238
239
240
241
242
243
244
245
246
247
248
249
250
251
252
253
254
255
256
257
258
259
260
261
262
263
264
265
266
267
268
269
270
271
272
273
274
275
276
277
278
279
280
281
282
283
284
285
286
287
288
289
290
291
292
293
294
295
296
297
298
299
300
301
302
303
304
305
306
307
308
309
310
311
312
313
314
315
316
317
318
319
320
321
322
323
324
325
326
327
328
329
330
331
332
333
334
335
336
337
338
339
340
341
342
343
344
345
346
347
348
349
350
351
352
353
354
355
356
357
358
359
360
361
362
363
364
365
366
367
368
369
370
371
372
373
374
375
376
377
378
379
380
381
382
383
384
385
386
387
388
389
390
391
392
393
394
395
396
397
398
399
400
401
402
403
404
405
406
407
408
409
410
411
412
413
414
415
416
417
418
419
420
421
422
423
424
425
426
427
428
429
430
431
432
433
434
435
436
437
438
439
440
441
442
443
444
445
446
447
448
449
450
451
452
453
454
455
456
457
458
459
460
461
462
463
464
465
466
467
468
469
470
471
472
473
474
475
476
477
478
479
480
481
482
483
484
485
486
487
488
489
490
491
492
493
494
495
496
497
498
499
500
501
502
503
504
505
506
507
508
509
510
511
512
513
514
515
516
517
518
519
520
521
522
523
524
525
526
527
528
529
530
531
532
533
534
535
536
537
538
539
540
541
542
543
544
545
546
547
548
549
550
551
552
553
554
555
556
557
558
559
560
561
562
563
564
565
566
567
568
569
570
571
572
573
574
575
576
577
578
579
580
581
582
583
584
585
586
587
588
589
590
591
592
593
594
595
596
597
598
599
600
601
602
603
604
605
606
607
608
609
610
611
612
613
614
615
616
617
618
619
620
621
622
623
624
625
626
627
628
629
630
631
632
633
634
635
636
637
638
639
640
641
642
643
644
645
646
647
648
649
650
651
652
653
654
655
656
657
658
659
660
661
662
663
664
665
666
667
668
669
670
671
672
673
674
675
676
677
678
679
680
681
682
683
684
685
686
687
688
689
690
691
692
693
694
695
696
697
698
699
700
701
702
703
704
705
706
707
708
709
710
711
712
713
714
715
716
717
718
719
720
721
722
723
724
725
726
727
728
729
730
731
732
733
734
735
736
737
738
739
740
741
742
743
744
745
746
747
748
749
750
751
752
753
754
755
756
757
758
759
760
761
762
763
764
765
766
767
768
769
770
771
772
773
774
775
776
777
778
779
780
781
782
783
784
785
786
787
788
789
790
791
792
793
794
795
796
797
798
799
800
801
802
803
804
805
806
807
808
809
810
811
812
813
814
815
816
817
818
819
820
821
822
823
824
825
826
827
828
829
830
831
832
833
834
835
836
837
838
839
840
841
842
843
844
845
846
847
848
849
850
851
852
853
854
855
856
857
858
859
860
861
862
863
864
865
866
867
868
869
870
871
872
873
874
875
876
877
878
879
880
881
882
883
884
885
886
887
888
889
890
891
892
893
894
895
896
897
898
899
900
901
902
903
904
905
906
907
908
909
910
911
912
913
914
915
916
917
918
919
920
921
922
923
924
925
926
927
928
929
930
931
932
933
934
935
936
937
938
939
940
941
942
943
944
945
946
947
948
949
950
951
952
953
954
955
956
957
958
959
960
961
962
963
964
965
966
967
968
969
970
971
972
973
974
975
976
977
978
979
980
981
982
983
984
985
986
987
988
989
990
991
992
993
994
995
996
997
998
999
1000

```

FIGURE 1

2/14

TATTTTCATGAGTTTGCAGTTGGTGGTAATACGGTTGAAGAATGGCTCTTGCCCTCATTT	50
M A L A P H S	7
CAAAATTTTCTGGCCCAACCATGAAACCATCAAAATATTATGTTGGGTCAAAGCTTCCCGGTC	120
N F L A N H E T I K Y Y V G S K L P G H	27
ATAAAAGGTTTAGCTGGGGTTGGGAAGATTACTTTGGTAGTATAGTCGTAGCAAAATTT	180
K R F S W G W E D Y F G S I V V A K I C	47
GTTCCAGCAGACGGATACCTAGATACTTTTGGAAATCTCTCTAGAAATATGCTGTGGTTGG	240
S S R R I P R Y F R K S P R I C C G L D	67
ATTCAAGAGGTTCTGCACTATTCTCACACGGGAACACAATCTCTCTCCCGCACATAGCA	300
S R G L Q L F S H G K H N L S P A H S I	87
TTAACCCAGAAATGTACCTAAGGGAAATTCAGGATGCAAAATTTCCAAAAGATGTAGCTTGA	360
N Q N V P K G N S G C K F P K D V A L M	107
TGGTTTGGGAGAAATGGGGCCAAATTTGCCAAACAGCAATGTAGCTATATTTCATTTCGT	420
V W E K W G Q F A K T A I V A I F I L S	127
CAGTTGCTTCAAAGCTGATGCGGTTGATGCTCTCAAGACTTGTACTTGGCTTACTGAAAG	480
V A S K A D A V D A L K T C T C L L K E	147
AGTGCAGGTTTAGAGCTTGGCAAGTGCATTTTCGAACCCCTGCATGTGCAGCTAATGTTGCGCT	540
C R L E L A K C I S N P A C A A N V A C	167
GTCTCCAGACTTGCACCAATAGACCTGACCAACCGGAATGTCAGATAAATGTGGTGAAT	600
L Q T C N N R P D E T E C Q I K C G D L	187
TGTTTGAAGAACAGTGTCTGTAGACGAGTTCAATGAGTGTGCAGTCTCCCGAAGAAATGTC	660
F E N S V V D E F N E C A V S R K K C V	207
TACCTCGTAAATCTGATGTTGGTGAAGTTTCCCTGTACCTGATCCCAAGTGTCTTGTCCAGA	720
P R K S D V G D F P V P D P S V L V Q K	227
AGTTTGACATGAAGATTTTACGCGGAATGGTTTCATTACTCCCGGTTTGAATCCCACTT	780
F D M K D F S G K W F I T R G L N P T F	247
TTGATGCTTTTGTATTGCCAATTGCATGAGTTCATACAGAAAGAAACAACTTGTGGGCA	840
D A F D C Q L H E F H T E E N K L V G K	267
ATTTATCTTGGAGATAAGTACACCTGATGGAGGATTTTCTACTCGATCAGCGGTGCAAA	900
L S N R I R T P D G G F F T R S A V Q K	287
AATTCGTGCAGATCCAAAGTATCCGGGGTACTCTACAAATCATGATGATGATGATGATGAT	960
F V Q D P K Y P G I L Y H H D N E Y L L	307
TCTACCAAGATGACTGGTATATTTTGGCATCCAAAGTAGAAATATAGTCCAGAGGATTACA	1020
Y Q D D W Y I L S S K Y E N S P E D Y I	327

FIGURE 2 1/2

TATTTGTGTACTATAAGGGCAGAAATGATGCATGGGATGGATATGGTGGTTCTGTACTTT	1080
F V Y Y K G R N D A W D G Y G G S V L Y	347
ACACAAGAAGTGCAGTTTTTGCCTGAAGCATTATACCGGAGTTGCAACCGCAGCTCAPP	1140
T R S A V L P E S I I P E L Q T A A Q X	367
AAGTTGGGGCGTGAATTTCAACACATTTCATAAAAACAGACAAATACAGTGGCCCTGAACCTC	1200
V G R D F N T F I K T D N T C G P E P P	387
CCCTTGTGTGACAGCTTGGAGAAAGTGGAAAGAGGAGAAAGGACGATCATAAAGGAG	1260
L V E R L E K K V E E G E R T E I K E V	407
TTGAGGAGATAGAAAGAAGTAGAGAAGGTGAGAGATAAAGAAGTCACCTTATTCAGTA	1320
E E I E E E V E K V R D K E V T L F S X	427
AAGTGTGTGAAGCTTTTAAAGAGCTCCAACGAGATGAAGAGAACTTCTTAAGAGAGCTGA	1380
L F E G F K E L Q R D E E N F L R E L S	447
GCAAGAAGAAATGGATGTTTTTGGATGGACTTAAATGGGAAGCAACTGAGGTAGAAAAAC	1440
K E E M D V L D G L K M E A T E V E K L	467
TTTTTGGGGCGTGCCTTACCAATAAGGAAATTAAGGTAAGTATTTTAAAACTATCAACAT	1500
F G R A L P I R K L R	478
ATACACTACATGTATAGTTGTATTTGATTCCTTTTGCCTGGAATAGATTGCTTATACATCA	1560
TGTATTCCTTCTTTTTCAGAAGCAAAAAA	1583

CCACGCGTCCGGCTTGGTGTGGGGAAGATTAGATAGTGTGAAGAATGGCAGTAGCTACAC	60
M A V A T H	6
ATTGTTTCACTTCACCTTGTCATGACCGTATTCGATTCTCTCAAGTGATGATGGTATTG	120
C F T S P C H D R I R F F S S D D G I G	26
GTAGGCTTGGCATTACAAGAAAGAGGATCAATGGCACCTTCTTGCTCAAGATTTTACCTC	180
R L G I T R K R I N G T F L L K I L P P	46
CAATCCAAAGTGCTGATCTCAGAACAACCTGGTGGGAGATCCTCACGTCCTTTATCTGCAT	240
I Q S A D L R T T G G R S S R P L S A F	66
TCAGGTGAGGATTCTCTAAGGGGATATTTGACATTGTGCCATTACCATCAAAGAATGAGC	300
R S G F S K G I F D I V P L P S K N E L	86
TGAAAGAGCTGACCGCTCCGCTGTTGCTAAACTCGTGGGTGTTTTAGCTTGCGCGTTCC	360
K E L T A P L L L K L V G V L A C A F L	106
TTATTGTTCCATCTGCAGATGCAGTTGATGCACCTAAACTTGTGCATGCTTATTGAAGG	420
I V P S A D A V D A L K T C A C L L K G	126
GATGCAGGATAGAACTCGCAAAGTGCAATGCCAACCTCGCTGTGCAGCCAATGTGCGCT	480
C R I E L A K C I A N P A C A A N V A C	146
GCCTTCAGACCTGCAATAACCGTCCAGATGAAACCGATGCCAGATTAAATGTGGGGATC	540
L Q T C N N R P D E T E C Q I K C G D L	166
TGTTTGAGAACAGTGTGTTGATGAGTTCAACGAGTGCTGTGTGCGAGAAAAAGTGTG	600
F E N S V V D E F N E C A V S R K K C V	186
TTCTAGAAAATCTGATCTCGGAGAATTTCTGCCCCGACCCCTTCTGTTCTGTACAGA	660
P R K S D L G E F P A P D P S V L V Q N	206
ACTTCAACATCTCGGACTTTAACGGAAGTGGTACATTAACAAGTGGCTTGAATCCAACCT	720
F N I S D F N G K W Y I T S G L N P T F	226
TTGATGCCTTCGACTGCCAGCTGCATGAGTTCCACACAGAAGGTGACAACAAGCTTGTG	780
D A F D C Q L H E F H T E G D N K L V G	246
GAAACATCTCTTGGAGAATAAAGACCCTAGACAGTGGATTCTTTACTAGGTGAGCCGTAC	840
N I S W R I K T L D S G F F T R S A V Q	266
AAAAATTCGTGCAAGATCCTAACCAACCTGGTGTCTCTACAATCATGACAACGAGTACC	900
K F V Q D P N Q P G V L Y N H D N E Y L	286
TTCATATCAAGATGACTGGTATATCCTGTCATCAAAATAGAGAATAAACCTGAAGACT	960
H Y Q D D W Y I L S S K I E N K P E D Y	306
ATATATTTGTATACTACCGTGGGCGAAACGATGCTTGATGGATATGGTGGTGCAGTTG	1020
I F V Y Y R G R N D A W D G Y G G A V V	326
TATACACGAGAAGTTCTGTATTACCCAATAGCATTATTCAGAACTCGAAAAAGCAGCAA	1080
Y T R S S V L P N S I I P E L E K A A K	346

FIGURE 3 1/2

AAAGCATAGGCAGAGACTTCAGCACATTCATTAGAACGATAACACATGTGGTCCTGAAC	1140
S I G R D F S T F I R T D N T C G P E P	366
CTGCGCTCGTGGAGAGAATTGAGAAGACAGTGAAGAAGGTGAAAGGATAATCGTAAAAG	1200
A L V E R I E K T V E E S E R I I V K E	386
AGGTTGAAGAGATAGAAGAAGAGGTAGAGAAGGAAGTGAGAAGGTCGGTAGGACTGAGA	1260
V E E I E E E V E K E V E K V G R T E M	406
TGACCTTGTTCCAGAGATTGGCTGAAGGATTTAATGAACTGAAGCAAGACGAGGAGAATT	1320
T L F Q R L A E G F N E L K Q D E E N F	426
TCGTGAGAGAGTTAAGTAAAGAAGAGATGGAGTTTTTGGATGAGATCAAAATGGAAGCAA	1380
V R E L S K E E M E F L D E I K M E A S	446
GTGAGGTTGAAAAATTGTTTGGGAAAGCTTTGCCAATCAGGAAGGTCAGGTAGAAACAAG	1440
E V E K L F G K A L P I R K V R *	462
AACCACCATTGTTGTACAAACTATATTATACATACTGTGTTCGGTTCATATAAAGTAATA	1500
TTTTTGTACACAGTCATCATCATTCATTAACAATTGGATAAAAAAAAAAAAAAAAAA	1555

6/14

Tobacco	MALAPHSNPLANHETIKYVVGSKLPQHCRPSWGWEDYFGSIVVAKICSSR	50
Arabidopsis	M-V-T-.....CFT-PCHDRI--PSS.D-GI-RLGITRK...P.	33
Lettuce	M--SL-TV--CKE-ALNL-AR-PCNE...--HRS.GQPPTN-IMM-....	43
Tobacco	RIPRYFRKSPRICCGLDNRGLQLF.SHGKHNLSPAHSINQNVKGNNGCR	99
Arabidopsis	--NGT-L..LK-LPPIQ-AD-RTGGRSSRP--APR-GPFGKIGFDIVPLP	81
Lettuce	-SNNGYFN-F-LFTSYKTSSF..SD-SHCKDK-QI.CSIDTSFEETQRFD	90
Tobacco	FPKDVAlMVWEKMGQFAKTAIVAIFILSVASKADA	134
Arabidopsis	SKNELKELTA...PLLL-LVG-LACAFLIVPS---	113
Lettuce	LKRGMT-1LEKQ-R--IQL---LVCTFVIVPRV--	125
Tobacco	VDALKTCTCLLKECRLELAKCISNPACAANVACLQTCNNRPDETECQIKC	50
Arabidopsis	-----A-----G-----I-----A-----	50
Lettuce	-----A-----I-----A-----S-----	50
Tobacco	GDLFENSVDDEFNECAVSHKKCVPRKSDVGDFFVPDPFVLVQKFDMDKDFS	100
Arabidopsis	-----L-E-A-----N-NIS--N	100
Lettuce	-----Q-----E-----RNAV--N-N-----	100
Tobacco	GKWFITRGLNPTFDAPDCQLHEPHE.EKLVGNLSWRIRTPDGGPFTAS	149
Arabidopsis	---Y-S-----GD-----I---K-L-S-----	150
Lettuce	---Y-S-----M-ND-----T---K-L-----	149
Tobacco	AVQKFVQDPKYPGILYNHENEYLLYQDDWYILSSKVENSPEDYIFVYKQ	199
Arabidopsis	-----NQ--V-----H-----I--K-----R	200
Lettuce	---T---DL--A-----F-H-----QI--K-D-----R	199
Tobacco	RNDAWDGYGGSVLYTRSAYLPESIIPELQTAQKVRDFNTFIKTDNTQG	249
Arabidopsis	-----A-V---S---N-----EK--KSI---S---R	250
Lettuce	-----I---PT-----N--K--KS-----N--T---S--	249
Tobacco	PEPPLVERLEKKVEEGERTIIKEVEEIEE...EVEKVRDKVTLFSKLF	295
Arabidopsis	---A---I--T-----I-V-----EVEK-----GRT-M---QR-A	300
Lettuce	-----TA---KLL---AV---EVEK-----T-M---QR-L	299
Tobacco	EGFKELQRDEENFLRELSKEEMDVLDGLRMEATEVEKLFGRALPIRKL	344
Arabidopsis	---N--KQ---V-----EP--EI---S-----K-----V-	349
Lettuce	-----Q---V-----KEI-NE-Q-----	348



A Cysteine-rich domain
 B Lipocalin signature
 C Highly charged domain

FIGURE 4

Percent Identity and Similarity* of Pre-protein VDE

	Lettuce	Tobacco	Arabidopsis
Lettuce		67 (78)	69 (82)
Tobacco	69	<i>protein cDNA</i>	68 (81)
Arabidopsis	66	68	

*similarity values are in parentheses

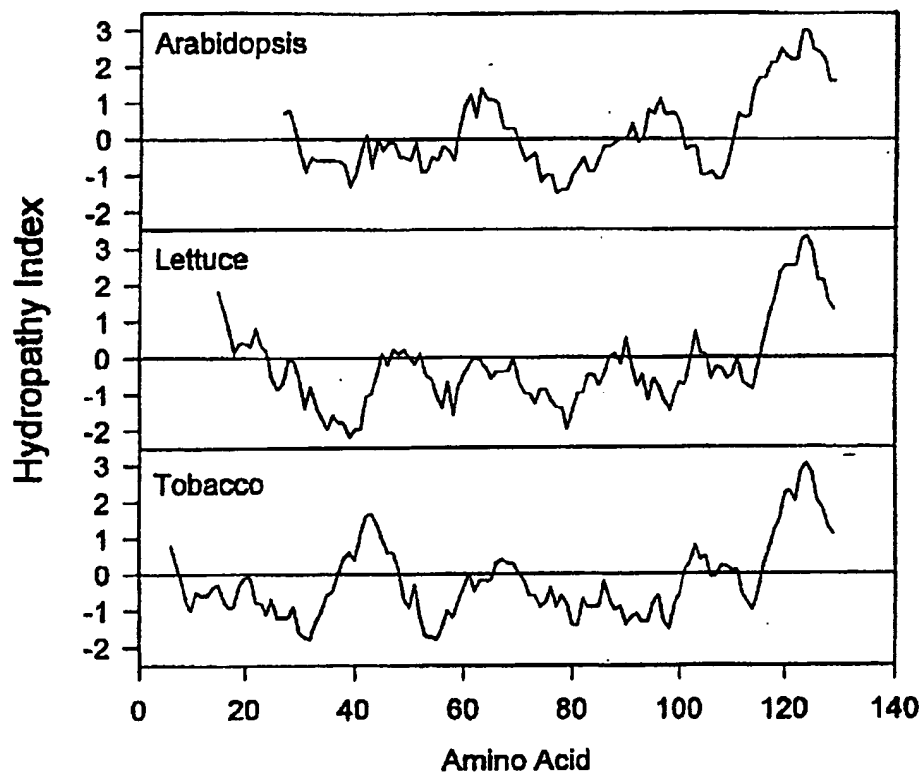
Percent Identity and Similarity* of Mature VDE

	Lettuce	Tobacco	Arabidopsis
Lettuce		82 (90)	83 (91)
Tobacco	76	<i>protein cDNA</i>	83 (92)
Arabidopsis	74	77	

*similarity values are in parentheses

FIGURE 5

8/14



Hydropathy profiles of the putative transit peptide for the three vde deduced polypeptide sequences using an average moving interval of 11 residues.

FIGURE 6

9/14

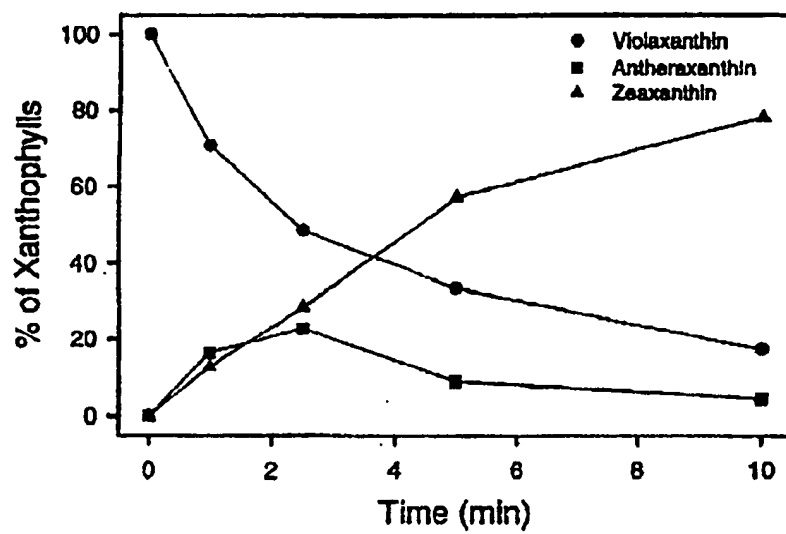
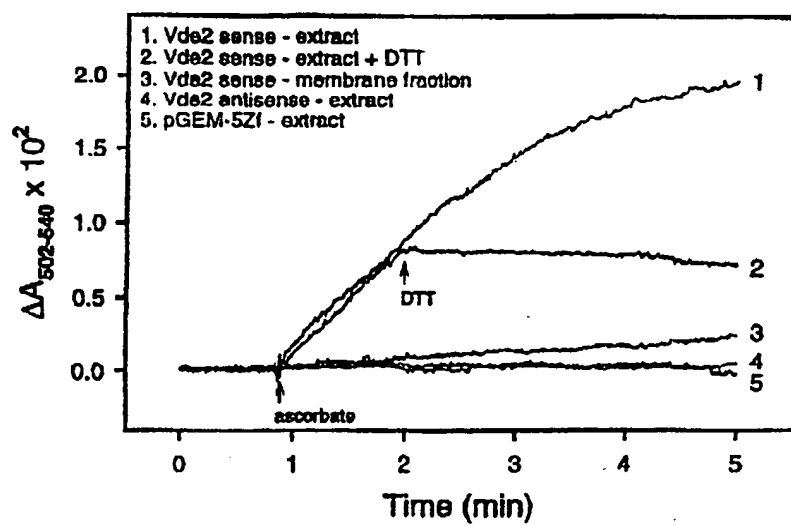


FIGURE 7

10/14

Plant	Treatment	N	V	A	Z	V+A+Z	L	Chlb/Chla	BB-Carotene	%V Desaponidized
Ct-11	Dark	77.19	64.67	1.54	0	66.21	336.12	0.39	136.85	60.5
	Light	77.65	25.58	6.25	30.93	62.74	338.15	0.40	131.78	
Ct-14	Dark	71.60	77.74	1.19	0	78.93	312.05	0.38	150.08	62.6
	Light	72.00	29.07	7.97	43.07	80.11	311.98	0.37	151.50	
Ct-15	Dark	76.88	67.44	0	0	67.44	345.73	0.43	130.05	60.4
	Light	74.45	26.73	7.78	37.44	71.95	337.87	0.42	128.98	
Ct-18	Dark	68.28	82.55	2.33	0	84.88	298.38	0.35	138.67	58.2
	Light	69.65	34.50	13.25	38.44	86.19	311.07	0.36	138.95	
Ct-20	Dark	78.45	70.60	2.85	0	73.45	351.57	0.39	139.58	67.2
	Light	77.38	23.14	5.46	42.66	71.26	343.25	0.39	133.81	
Ct-22	Dark	72.68	104.14	3.40	0	107.54	323.93	0.37	138.29	73.5
	Light	72.13	27.63	6.82	78.66	112.91	315.07	0.40	128.30	
Ct-24	Dark	70.77	76.82	1.55	0	78.37	334.20	0.43	132.95	61.8
	Light	76.52	29.35	7.92	45.24	82.51	339.60	0.44	131.55	
Ct-26	Dark	75.28	63.41	0	0	63.41	348.45	0.44	130.38	58.6
	Light	77.34	26.27	6.16	34.18	66.62	346.81	0.44	128.27	
Ct-30	Dark	78.23	59.68	1.73	0	61.39	357.53	0.45	127.52	55.8
	Light	79.37	26.47	4.93	31.81	63.01	352.39	0.46	124.80	
Ct-31	Dark	71.72	75.91	1.74	0	77.65	315.40	0.37	144.24	58.6
	Light	73.00	31.43	8.74	37.65	77.82	312.60	0.38	145.13	
Ct-39	Dark	75.99	77.93	0	0	77.93	335.79	0.43	127.17	66.3
	Light	74.78	26.28	8.07	41.30	75.65	331.35	0.42	123.11	
Ct-40	Dark	77.58	78.07	2.99	0	82.06	358.33	0.44	126.05	65.3
	Light	77.78	27.44	10.10	47.82	85.46	352.66	0.43	120.89	

Mean = 62.4 ± 5.0

N = 9'-cis-neoxanthin V = violaxanthin A = antheraxanthin Z = zeaxanthin L = lutein Chla = chlorophyll a Chlb = chlorophyll b

All values are relative to chlorophyll a (nmol mol⁻¹ Chla) except Chlb/Chla which is (mol/mol).

FIGURE 8

1/3

Plant	Treatment	N	V	A	Z	V+A+Z	L	Chl _a /Chl _b	88-Carotene	%V De-epoxidized	% Inhibition of De-epoxidation
TAS-32	Dark	74.19	78.98	0	0	78.98	325.75	0.42	138.45		94.1
	Light	73.78	74.15	2.18	0	76.33	330.95	0.41	131.73	3.7	
TAS-39	Dark	77.92	58.19	0	0	59.19	329.29	0.41	141.45		82.5
	Light	75.08	56.39	2.70	0	59.09	322.29	0.40	141.52	4.7	
TAS-21	Dark	75.78	53.19	0	0	53.19	335.21	0.45	132.85		72.0
	Light	77.92	43.90	7.30	9.37	60.57	328.90	0.45	130.33	17.5	
TAS-5	Dark	67.82	79.21	3.43	0	82.64	300.82	0.39	139.00		65.9
	Light	69.72	62.31	14.68	8.27	85.24	300.63	0.40	137.13	21.3	
TAS-17	Dark	74.89	64.54	1.08	0	65.62	317.69	0.41	143.42		63.6
	Light	74.00	49.89	8.49	8.53	68.91	325.32	0.40	139.28	22.7	
TAS-13	Dark	77.92	49.33	1.27	0	50.60	339.63	0.45	135.38		62.7
	Light	78.02	37.82	4.94	7.18	49.94	340.45	0.45	132.78	23.3	
TAS-6	Dark	74.42	55.77	0	0	55.77	340.84	0.44	136.77		55.4
	Light	74.95	40.27	9.69	13.99	63.95	332.00	0.44	135.38	27.8	
TAS-37	Dark	73.05	59.18	1.24	0	60.42	323.30	0.39	135.81		45.3
	Light	71.36	38.97	14.48	9.98	63.43	313.46	0.38	134.62	34.1	
TAS-3	Dark	74.04	60.25	1.76	0	62.01	318.39	0.43	138.89		44.2
	Light	76.98	38.28	7.41	14.33	61.00	322.14	0.44	136.00	34.8	
TAS-36	Dark	69.77	77.86	1.42	0	79.28	295.52	0.36	151.33		40.1
	Light	70.74	48.73	12.76	12.81	74.30	308.08	0.36	151.35	37.4	
TAS-35	Dark	75.59	63.24	1.05	0	64.29	342.09	0.42	130.30		39.7
	Light	75.78	39.48	10.38	17.49	67.35	337.57	0.42	128.88	37.8	
TAS-4	Dark	73.61	68.23	1.31	0	69.54	321.12	0.42	135.43		38.6
	Light	73.23	42.07	8.95	17.84	68.88	320.33	0.42	131.73	38.3	
TAS-9	Dark	72.28	52.57	1.75	0	54.32	324.02	0.42	140.21		38.4
	Light	73.28	31.72	6.19	18.59	56.50	317.11	0.42	138.33	39.7	

FIGURE 8

TAS-7	Dark	72.55	71.02	1.81	0	72.83	321.37	0.40	133.21	43.9	29.6
	Light	71.79	99.82	14.04	21.09	74.95	322.04	0.40	130.57		
TAS-38	Dark	71.68	61.97	1.77	0	63.74	329.67	0.41	135.87	44.4	28.8
	Light	73.24	34.45	6.83	19.57	62.85	331.17	0.41	133.77		
TAS-16	Dark	72.15	62.54	2.04	0	64.58	329.72	0.41	135.12	46.8	25.0
	Light	74.04	33.28	9.10	23.83	68.21	335.60	0.42	131.32		
TAS-18	Dark	75.09	59.64	1.72	0	61.38	345.04	0.42	127.38	46.8	24.8
	Light	75.28	31.68	7.11	23.01	61.80	340.79	0.42	128.85		
TAS-34	Dark	72.35	65.39	1.79	0	67.18	326.06	0.41	131.12	47.6	23.7
	Light	71.25	34.26	8.26	30.41	73.93	318.49	0.42	128.96		

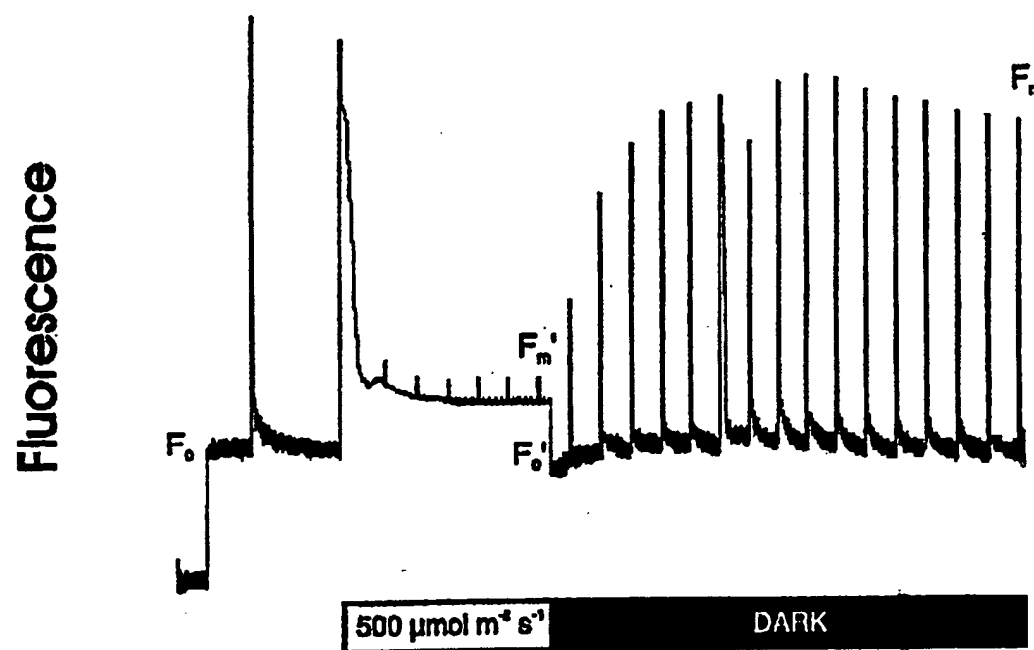
N = 9'-cis-neoxanthin V = violaxanthin A = antheraxanthin Z = zeaxanthin L = lutein Chla = chlorophyll a Chlb = chlorophyll b

All values are relative to chlorophyll a (mmol mol⁻¹ Chla) except Chlb/Chla which is (mol/mol).

FIGURE 8C

13/14

Ct-30

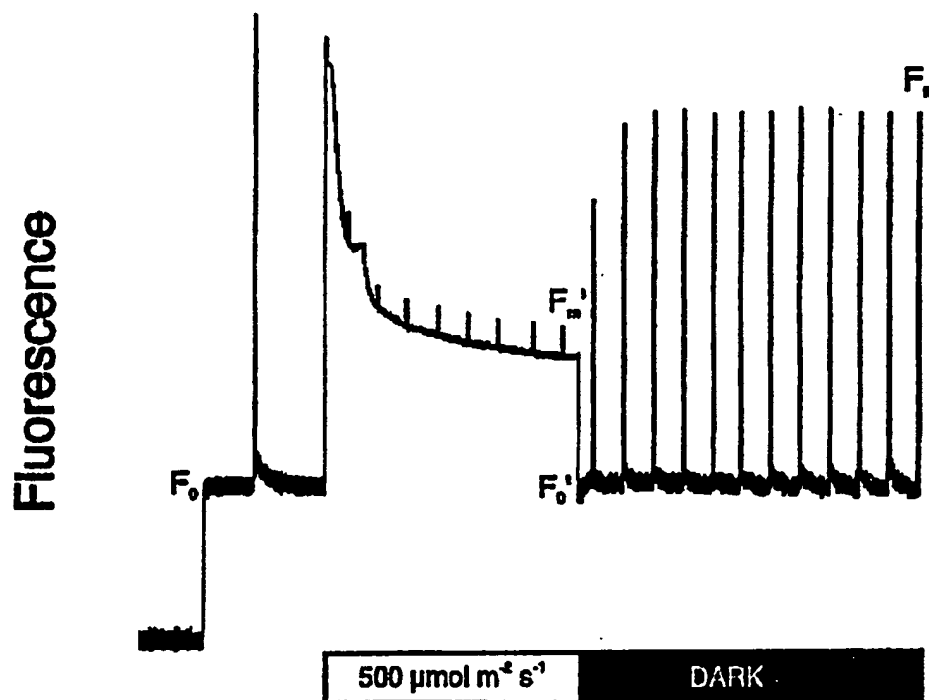


	Dark-adapted	Pre-illuminated	Post-fluorescence Analysis
V	64.28	51.77	44.98
A	1.99	6.16	11.10
Z	0	10.17	13.77
V+A+Z	66.27	68.10	69.85
De-epoxidation (%)		19.5	30.00
$(F_m/F_m') - 1$			2.20
$(F_0/F_0') - 1$			0.15

All values are relative to chlorophyll *a* ($\text{mmol mol}^{-1} \text{Chla}$).

FIGURE 9

TAS-5



	Dark-adapted	Pre-illuminated	Post-fluorescence Analysis
V	67.51	NA	65.38
A	0	NA	2.14
Z	0	NA	0
V+A+Z	67.51	NA	67.52
De-epoxidation (%)		NA	3.20
$(F_m/F_m') - 1$			1.34
$(F_0/F_0') - 1$			0

All values are relative to chlorophyll *a* ($\mu\text{mol mol}^{-1}$ Chla).

NA - Not assayed

FIGURE 10

PCTWORLD INTELLECTUAL PROPERTY ORGANIZATION
International Bureau

INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(51) International Patent Classification ⁶ : C12N 15/29, 15/53, 15/82, 5/10, A01H 1/00, 5/00	A3	(11) International Publication Number: WO 97/17447 (43) International Publication Date: 15 May 1997 (15.05.97)
(21) International Application Number: PCT/US96/18291 (22) International Filing Date: 7 November 1996 (07.11.96) (30) Priority Data: 60/006,315 7 November 1995 (07.11.95) US 60/023,502 6 August 1996 (06.08.96) US (71) Applicant: CALGENE, INC. [US/US]; 1920 Fifth Street, Davis, CA 95616 (US). (72) Inventors: YAMAMOTO, Harry, Y.; 716 Pao Street, Honolulu, HI 96825 (US). BUGOS, Robert, C.; 2135 Chamberlain Street, Honolulu, HI 96822 (US). ROCKHOLM, David, C.; 1704 Anapuni Street, Honolulu, HI 96822 (US). (74) Agents: SCHWEDLER, Carl, J. et al.; Calgene, Inc., 1920 Fifth Street, Davis, CA 95616 (US).		(81) Designated States: CA, JP, MX, European patent (AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE). Published <i>With international search report.</i> <i>Before the expiration of the time limit for amending the claims and to be republished in the event of the receipt of amendments.</i> (88) Date of publication of the International search report: 9 October 1997 (09.10.97)
(54) Title: PLANT VDE GENES AND METHODS RELATED THERETO (57) Abstract DNA sequences encoding plant vde enzymes are provided herein. The sequences may be joined to heterologous DNA sequences for use as probes and in DNA constructs to modify the genotype of a host organism. DNA constructs and methods are provided to modify a host cell phenotype by altering the amount of photoprotection enzyme present in the host cell. In plastid containing host cells, zeaxanthin levels and sensitivity to light can be modified through alterations in the level of vde enzymes.		

FOR THE PURPOSES OF INFORMATION ONLY

Codes used to identify States party to the PCT on the front pages of pamphlets publishing international applications under the PCT.

AM	Armenia	GB	United Kingdom	MW	Malawi
AT	Austria	GE	Georgia	MX	Mexico
AU	Australia	GN	Guinea	NE	Niger
BB	Barbados	GR	Greece	NL	Netherlands
BE	Belgium	HU	Hungary	NO	Norway
BF	Burkina Faso	IE	Ireland	NZ	New Zealand
BG	Bulgaria	IT	Italy	PL	Poland
BJ	Benin	JP	Japan	PT	Portugal
BR	Brazil	KE	Kenya	RO	Romania
BY	Belarus	KG	Kyrgyzstan	RU	Russian Federation
CA	Canada	KP	Democratic People's Republic of Korea	SD	Sudan
CF	Central African Republic			SE	Sweden
CG	Congo	KR	Republic of Korea	SG	Singapore
CH	Switzerland	KZ	Kazakhstan	SI	Slovenia
CI	Côte d'Ivoire	LI	Liechtenstein	SK	Slovakia
CM	Cameroon	LK	Sri Lanka	SN	Senegal
CN	China	LR	Liberia	SZ	Swaziland
CS	Czechoslovakia	LT	Lithuania	TD	Chad
CZ	Czech Republic	LU	Luxembourg	TG	Togo
DE	Germany	LV	Latvia	TJ	Tajikistan
DK	Denmark	MC	Monaco	TT	Trinidad and Tobago
EE	Estonia	MD	Republic of Moldova	UA	Ukraine
ES	Spain	MG	Madagascar	UG	Uganda
FI	Finland	ML	Mali	US	United States of America
FR	France	MN	Mongolia	UZ	Uzbekistan
GA	Gabon	MR	Mauritania	VN	Viet Nam

INTERNATIONAL SEARCH REPORT

Intern. Appl. Application No PCT/US 96/18291		
A. CLASSIFICATION OF SUBJECT MATTER IPC 6 C12N15/29 C12N15/53 C12N15/82 C12N5/10 A01H1/00 A01H5/00		
According to International Patent Classification (IPC) or to both national classification and IPC		
B. FIELDS SEARCHED Minimum documentation searched (classification system followed by classification symbols) IPC 6 C07K C12N A01H		
Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched		
Electronic data base consulted during the international search (name of data base and, where practical, search terms used)		
C. DOCUMENTS CONSIDERED TO BE RELEVANT		
Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
P,X	PROC. NATL. ACAD. SCI. USA, vol. 93, no. 13, 25 June 1996, pages 6320-6325, XP002036884 BUGOS, R.C. AND YAMAMOTO, H.Y.: "Molecular cloning of violaxanthin de-epoxidase from romaine lettuce and expression in Escherichia coli"	1,2,4-8
P,Y	see the whole document ---	3,9-22
P,X	DATABASE EMBL Entry Empln:Ntu34817, Accession number U34817, 27 July 1996 XP002036887 see abstract & UNPUBLISHED, BUGOS, R.C. AND YAMAMOTO, H.Y.: "Nicotiana tabacum violaxanthin de-epoxidase precursor (TVDE1)" ---	1,4-8
-/--		
<div style="display: flex; justify-content: space-between;"> <input checked="" type="checkbox"/> Further documents are listed in the continuation of box C. <input checked="" type="checkbox"/> Patent family members are listed in annex. </div>		
* Special categories of cited documents : <div style="display: flex;"> <div style="flex: 1;"> <p>"A" document defining the general state of the art which is not considered to be of particular relevance</p> <p>"E" earlier document but published on or after the international filing date</p> <p>"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)</p> <p>"O" document referring to an oral disclosure, use, exhibition or other means</p> <p>"P" document published prior to the international filing date but later than the priority date claimed</p> </div> <div style="flex: 1;"> <p>"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention</p> <p>"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone</p> <p>"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art.</p> <p>"&" document member of the same patent family</p> </div> </div>		
Date of the actual completion of the international search <div style="text-align: center;">8 August 1997</div>		Date of mailing of the international search report <div style="text-align: center;">26.08.97</div>
Name and mailing address of the ISA European Patent Office, P.B. 5818 Patentlaan 2 NL - 2280 HV Rijswijk Tel. (+31-70) 340-2040, Tx. 31 651 epo nl, Fax (+31-70) 340-3016		Authorized officer <div style="text-align: center;">Donath, C</div>

INTERNATIONAL SEARCH REPORT

Intern. Application No
PCT/US 96/18291

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
P,X	<p>DATABASE EMBL Entry Empln:Atu44133, Accession number U44133, 28 July 1996 XP002036888 see abstract & UNPUBLISHED, BUGOS, R.C. AND YAMAMOTO, H.Y.: "Arabidopsis thaliana violaxanthin de-epoxidase precursor (AVDE1)" ---</p>	1,4-8
P,Y	<p>PLANT PHYSIOL., vol. 110, 1996, pages 697-703, XP002036885 ROCKHOLM, D.C. AND YAMAMOTO, H.Y.: "Violaxanthin de-epoxidase" cited in the application see the whole document ---</p>	3,9-22
A	<p>METHODS IN ENZYMOLOGY, vol. 110, 1985, pages 303-312, XP002036886 YAMAMOTO, H.Y.: "Xanthophyll cycles" see page 307, last paragraph - page 312, last paragraph ---</p>	1-22
A	<p>WO 92 11382 A (CALGENE, INC.) 9 July 1992 see the whole document -----</p>	9-22

Information on patent family members

PCT/US 96/18291

Form PCT/ISA/210 (patent family annex) (July 1992)